

Sequence Listing

<110> Desnoyers,Luc

Eaton,Dan L.

Goddard,Audrey

Godowski,Paul J.

Gurney,Austin L.

Pan,James

Stewart,Timothy A.

Watanabe,Colin K.

Wood,William I.

Zhang,Zemin

<120> SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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Gln	Thr	Gly	Gly	Leu	Pro	Pro	Asp	Cys	Ser	Lys	Cys	Cys	His	Gly
				35					40					45
Asp	Tyr	Ser	Phe	Arg	Gly	Tyr	Gln	Gly	Pro	Pro	Gly	Pro	Pro	Gly
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Pro	Pro	Gly	Ile	Pro	Gly	Asn	His	Gly	Asn	Asn	Gly	Asn	Asn	Gly
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Asp	Leu	Gly	Pro	Arg	Gly	Glu	Arg	Gly	Gln	His	Gly	Pro	Lys	Gly
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Glu	Lys	Gly	Tyr	Pro	Gly	Ile	Pro	Pro	Glu	Leu	Gln	Ile	Ala	Phe
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Met	Ala	Ser	Leu	Ala	Thr	His	Phe	Ser	Asn	Gln	Asn	Ser	Gly	Ile
				125					130					135
Ile	Phe	Ser	Ser	Val	Glu	Thr	Asn	Ile	Gly	Asn	Phe	Phe	Asp	Val
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Thr	Phe	Ser	Met	Met	Lys	His	Glu	Asp	Val	Glu	Glu	Val	Tyr	Val
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Tyr	Leu	Met	His	Asn	Gly	Asn	Thr	Val	Phe	Ser	Met	Tyr	Ser	Tyr
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Glu	Met	Lys	Gly	Lys	Ser	Asp	Thr	Ser	Ser	Asn	His	Ala	Val	Leu
				200					205					210
Lys	Leu	Ala	Lys	Gly	Asp	Glu	Val	Trp	Leu	Arg	Met	Gly	Asn	Gly
				215					220					225
Ala	Leu	His	Gly	Asp	His	Gln	Arg	Phe	Ser	Thr	Phe	Ala	Gly	Phe
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cc 52

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<213> Homo Sapien

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Leu	Asp	Gly	Phe	Arg	Ser	Asp	Tyr	Ile	Ser	Asp	Glu	Ala	Leu	Glu	35	40	45	
Ser	Leu	Pro	Gly	Phe	Lys	Glu	Ile	Val	Ser	Arg	Gly	Val	Lys	Val	50	55	60	
Asp	Tyr	Leu	Thr	Pro	Asp	Phe	Pro	Ser	Leu	Ser	Tyr	Pro	Asn	Tyr	65	70	75	
Tyr	Thr	Leu	Met	Thr	Gly	Arg	His	Cys	Glu	Val	His	Gln	Met	Ile	80	85	90	
Gly	Asn	Tyr	Met	Trp	Asp	Pro	Thr	Thr	Asn	Lys	Ser	Phe	Asp	Ile	95	100	105	
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Glu Pro Leu Trp	Val Thr Leu Thr Lys	Ala Lys Arg Lys Val Tyr			
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Pro Thr Tyr Cys	Leu Glu Tyr Lys Asn	Val Pro Thr Asp Ile Asn			
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Phe Ala Asn Ala	Val Ser Asp Ala Leu	Asp Ser Phe Lys Ser Gly			
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Arg Ala Asp Leu	Ala Ala Ile Tyr His	Glu Arg Ile Asp Val Glu			
	185	190			195
Gly His His Tyr	Gly Pro Ala Ser Pro	Gln Arg Lys Asp Ala Leu			
	200	205			210
Lys Ala Val Asp	Thr Val Leu Lys Tyr	Met Thr Lys Trp Ile Gln			
	215	220			225
Glu Arg Gly Leu	Gln Asp Arg Leu Asn	Val Ile Ile Phe Ser Asp			
	230	235			240
His Gly Met Thr	Asp Ile Phe Trp Met	Asp Lys Val Ile Glu Leu			
	245	250			255
Asn Lys Tyr Ile	Ser Leu Asn Asp Leu	Gln Gln Val Lys Asp Arg			
	260	265			270
Gly Pro Val Val	Ser Leu Trp Pro Ala	Pro Gly Lys His Ser Glu			
	275	280			285
Ile Tyr Asn Lys	Leu Ser Thr Val Glu	His Met Thr Val Tyr Glu			
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Lys Glu Ala Ile	Pro Ser Arg Phe Tyr	Tyr Lys Lys Gly Lys Phe			
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Val Ser Pro Leu	Thr Leu Val Ala Asp	Glu Gly Trp Phe Ile Thr			
	320	325			330
Glu Asn Arg Glu	Met Leu Pro Phe Trp	Met Asn Ser Thr Gly Arg			
	335	340			345
Arg Glu Gly Trp	Gln Arg Gly Trp His	Gly Tyr Asp Asn Glu Leu			
	350	355			360
Met Asp Met Arg	Gly Ile Phe Leu Ala	Phe Gly Pro Asp Phe Lys			
	365	370			375
Ser Asn Phe Arg	Ala Ala Pro Ile Arg	Ser Val Asp Val Tyr Asn			
	380	385			390
Val Met Cys Asn	Val Val Gly Ile Thr	Pro Leu Pro Asn Asn Gly			
	395	400			405

Ser Trp Ser Arg Val Met Cys Met Leu Lys Gly Arg Ala Gly Thr
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His	Gly	Thr	Pro	His	Cys	Tyr	Ser	Ala	Glu	Glu	Leu	Pro	Leu	Gly	35	40	45	
Gln	Ala	Pro	Pro	His	Leu	Leu	Ala	Arg	Gly	Ala	Lys	Trp	Gly	Gln	50	55	60	
Ala	Leu	Pro	Val	Ala	Leu	Val	Ser	Ser	Leu	Glu	Ala	Ala	Ser	His	65	70	75	
Arg	Gly	Arg	His	Glu	Arg	Pro	Ser	Ala	Thr	Thr	Gln	Cys	Pro	Val	80	85	90	
Leu	Arg	Pro	Glu	Glu	Val	Leu	Glu	Ala	Asp	Thr	His	Gln	Arg	Ser	95	100	105	
Ile	Ser	Pro	Trp	Arg	Tyr	Arg	Val	Asp	Thr	Asp	Glu	Asp	Arg	Tyr	110	115	120	
Pro	Gln	Lys	Leu	Ala	Phe	Ala	Glu	Cys	Leu	Cys	Arg	Gly	Cys	Ile	125	130	135	
Asp	Ala	Arg	Thr	Gly	Arg	Glu	Thr	Ala	Ala	Leu	Asn	Ser	Val	Arg	140	145	150	
Leu	Leu	Gln	Ser	Leu	Leu	Val	Leu	Arg	Arg	Arg	Pro	Cys	Ser	Arg	155	160	165	
Asp	Gly	Ser	Gly	Leu	Pro	Thr	Pro	Gly	Ala	Phe	Ala	Phe	His	Thr	170	175	180	
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gggacgtgga tgaactcggg gtgg 24

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<213> Homo Sapien

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35 40 45
His Cys Val Thr Thr Ala Thr Arg Val Leu Ser Asn Thr Glu Asp
50 55 60
Leu Pro Leu Val Thr Lys Met Cys His Ile Gly Cys Pro Asp Ile
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Pro Ser Leu Gly Leu Gly Pro Tyr Val Ser Ile Ala Cys Cys Gln
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Thr Ser Leu Cys Asn His Asp
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<210> 18
 <211> 273
 <212> PRT
 <213> Homo Sapien

<400> 18
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 Cys Phe Ala Asp Phe Lys His Pro Cys Tyr Lys Met Ala Tyr Phe
 35 40 45
 His Glu Leu Ser Ser Arg Val Ser Phe Gln Glu Ala Arg Leu Ala
 50 55 60
 Cys Glu Ser Glu Gly Gly Val Leu Leu Ser Leu Glu Asn Glu Ala
 65 70 75
 Glu Gln Lys Leu Ile Glu Ser Met Leu Gln Asn Leu Thr Lys Pro
 80 85 90
 Gly Thr Gly Ile Ser Asp Gly Asp Phe Trp Ile Gly Leu Trp Arg
 95 100 105
 Asn Gly Asp Gly Gln Thr Ser Gly Ala Cys Pro Asp Leu Tyr Gln
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 Trp Ser Asp Gly Ser Asn Ser Gln Tyr Arg Asn Trp Tyr Thr Asp
 125 130 135
 Glu Pro Ser Cys Gly Ser Glu Lys Cys Val Val Met Tyr His Gln
 140 145 150
 Pro Thr Ala Asn Pro Gly Leu Gly Gly Pro Tyr Leu Tyr Gln Trp
 155 160 165
 Asn Asp Asp Arg Cys Asn Met Lys His Asn Tyr Ile Cys Lys Tyr

	170		175		180
Glu Pro Glu Ile	Asn Pro Thr Ala Pro	Val Glu Lys Pro Tyr	Leu		
	185		190		195
Thr Asn Gln Pro	Gly Asp Thr His Gln	Asn Val Val Val Thr	Glu		
	200		205		210
Ala Gly Ile Ile	Pro Asn Leu Ile Tyr	Val Val Ile Pro Thr	Ile		
	215		220		225
Pro Leu Leu Leu	Leu Ile Leu Val Ala	Phe Gly Thr Cys Cys	Phe		
	230		235		240
Gln Met Leu His	Lys Ser Lys Gly Arg	Thr Lys Thr Ser Pro	Asn		
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Met Glu Val					

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 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 19
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<210> 20
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 20
 accacattct gatgggtgtc tcctgg 26

<210> 21
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 21
 gggtcctac cttaccagt ggaatgatga caggtgtaac atgaagcac 49

<210> 22
 <211> 3824

<212> DNA
<213> Homo Sapien

<400> 22

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 aataaatctt gctactgccc aaaa 3824

<210> 23
 <211> 571
 <212> PRT
 <213> Homo Sapien

<400> 23
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 Val Cys Leu Leu Leu Ala Cys Pro Ala Thr Ala Thr Gly Pro Glu
 20 25 30
 Val Ala Gln Pro Glu Val Asp Thr Thr Leu Gly Arg Val Arg Gly
 35 40 45
 Arg Gln Val Gly Val Lys Gly Thr Asp Arg Leu Val Asn Val Phe

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Leu	Gly	Ile	Pro	Phe	Ala	Gln	Pro	Pro	Leu	Gly	Pro	Asp	Arg	Phe	
				65					70					75	
Ser	Ala	Pro	His	Pro	Ala	Gln	Pro	Trp	Glu	Gly	Val	Arg	Asp	Ala	
				80					85					90	
Ser	Thr	Ala	Pro	Pro	Met	Cys	Leu	Gln	Asp	Val	Glu	Ser	Met	Asn	
				95					100					105	
Ser	Ser	Arg	Phe	Val	Leu	Asn	Gly	Lys	Gln	Gln	Ile	Phe	Ser	Val	
				110					115					120	
Ser	Glu	Asp	Cys	Leu	Val	Leu	Asn	Val	Tyr	Ser	Pro	Ala	Glu	Val	
				125					130					135	
Pro	Ala	Gly	Ser	Gly	Arg	Pro	Val	Met	Val	Trp	Val	His	Gly	Gly	
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Ala	Leu	Ile	Thr	Gly	Ala	Ala	Thr	Ser	Tyr	Asp	Gly	Ser	Ala	Leu	
				155					160					165	
Ala	Ala	Tyr	Gly	Asp	Val	Val	Val	Val	Thr	Val	Gln	Tyr	Arg	Leu	
				170					175					180	
Gly	Val	Leu	Gly	Phe	Phe	Ser	Thr	Gly	Asp	Glu	His	Ala	Pro	Gly	
				185					190					195	
Asn	Gln	Gly	Phe	Leu	Asp	Val	Val	Ala	Ala	Leu	Arg	Trp	Val	Gln	
				200					205					210	
Glu	Asn	Ile	Ala	Pro	Phe	Gly	Gly	Asp	Leu	Asn	Cys	Val	Thr	Val	
				215					220					225	
Phe	Gly	Gly	Ser	Ala	Gly	Gly	Ser	Ile	Ile	Ser	Gly	Leu	Val	Leu	
				230					235					240	
Ser	Pro	Val	Ala	Ala	Gly	Leu	Phe	His	Arg	Ala	Ile	Thr	Gln	Ser	
				245					250					255	
Gly	Val	Ile	Thr	Thr	Pro	Gly	Ile	Ile	Asp	Ser	His	Pro	Trp	Pro	
				260					265					270	
Leu	Ala	Gln	Lys	Ile	Ala	Asn	Thr	Leu	Ala	Cys	Ser	Ser	Ser	Ser	
				275					280					285	
Pro	Ala	Glu	Met	Val	Gln	Cys	Leu	Gln	Gln	Lys	Glu	Gly	Glu	Glu	
				290					295					300	
Leu	Val	Leu	Ser	Lys	Lys	Leu	Lys	Asn	Thr	Ile	Tyr	Pro	Leu	Thr	
				305					310					315	
Val	Asp	Gly	Thr	Val	Phe	Pro	Lys	Ser	Pro	Lys	Glu	Leu	Leu	Lys	
				320					325					330	
Glu	Lys	Pro	Phe	His	Ser	Val	Pro	Phe	Leu	Met	Gly	Val	Asn	Asn	
				335					340					345	

His	Glu	Phe	Ser	Trp	Leu	Ile	Pro	Arg	Gly	Trp	Gly	Leu	Leu	Asp	350	355	360
Thr	Met	Glu	Gln	Met	Ser	Arg	Glu	Asp	Met	Leu	Ala	Ile	Ser	Thr	365	370	375
Pro	Val	Leu	Thr	Ser	Leu	Asp	Val	Pro	Pro	Glu	Met	Met	Pro	Thr	380	385	390
Val	Ile	Asp	Glu	Tyr	Leu	Gly	Ser	Asn	Ser	Asp	Ala	Gln	Ala	Lys	395	400	405
Cys	Gln	Ala	Phe	Gln	Glu	Phe	Met	Gly	Asp	Val	Phe	Ile	Asn	Val	410	415	420
Pro	Thr	Val	Ser	Phe	Ser	Arg	Tyr	Leu	Arg	Asp	Ser	Gly	Ser	Pro	425	430	435
Val	Phe	Phe	Tyr	Glu	Phe	Gln	His	Arg	Pro	Ser	Ser	Phe	Ala	Lys	440	445	450
Ile	Lys	Pro	Ala	Trp	Val	Lys	Ala	Asp	His	Gly	Ala	Glu	Gly	Ala	455	460	465
Phe	Val	Phe	Gly	Gly	Pro	Phe	Leu	Met	Asp	Glu	Ser	Ser	Arg	Leu	470	475	480
Ala	Phe	Pro	Glu	Ala	Thr	Glu	Glu	Glu	Lys	Gln	Leu	Ser	Leu	Thr	485	490	495
Met	Met	Ala	Gln	Trp	Thr	His	Phe	Ala	Arg	Thr	Gly	Asp	Pro	Asn	500	505	510
Ser	Lys	Ala	Leu	Pro	Pro	Trp	Pro	Gln	Phe	Asn	Gln	Ala	Glu	Gln	515	520	525
Tyr	Leu	Glu	Ile	Asn	Pro	Val	Pro	Arg	Ala	Gly	Gln	Lys	Phe	Arg	530	535	540
Glu	Ala	Trp	Met	Gln	Phe	Trp	Ser	Glu	Thr	Leu	Pro	Ser	Lys	Ile	545	550	555
Gln	Gln	Trp	His	Gln	Lys	Gln	Lys	Asn	Arg	Lys	Ala	Gln	Glu	Asp	560	565	570

Leu

<210> 24

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 24

gcaaagctct gcctccttgg cc 22

<210> 25
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 25
gggtggactg tgctctaata gacgc 25

<210> 26
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 26
cgtggcactg ggttgatc 18

<210> 27
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 27
gatgcagttc tggtcagaga cgctccccag caagatacaa cagtg 45

<210> 28
<211> 1342
<212> DNA
<213> Homo Sapien

<400> 28
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<210> 29
 <211> 209
 <212> PRT
 <213> Homo Sapien

<400> 29
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 Thr Leu Phe Leu Leu Gln Leu Lys Phe Leu Lys Pro Lys Ile Asn
 35 40 45
 Ser Phe Tyr Ala Phe Glu Val Lys Asp Ala Lys Gly Arg Thr Val
 50 55 60
 Ser Leu Glu Lys Tyr Lys Gly Lys Val Ser Leu Val Val Asn Val
 65 70 75
 Ala Ser Asp Cys Gln Leu Thr Asp Arg Asn Tyr Leu Gly Leu Lys
 80 85 90

Glu	Leu	His	Lys	Glu	Phe	Gly	Pro	Ser	His	Phe	Ser	Val	Leu	Ala
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Phe	Pro	Cys	Asn	Gln	Phe	Gly	Glu	Ser	Glu	Pro	Arg	Pro	Ser	Lys
				110					115					120
Glu	Val	Glu	Ser	Phe	Ala	Arg	Lys	Asn	Tyr	Gly	Val	Thr	Phe	Pro
				125					130					135
Ile	Phe	His	Lys	Ile	Lys	Ile	Leu	Gly	Ser	Glu	Gly	Glu	Pro	Ala
				140					145					150
Phe	Arg	Phe	Leu	Val	Asp	Ser	Ser	Lys	Lys	Glu	Pro	Arg	Trp	Asn
				155					160					165
Phe	Trp	Lys	Tyr	Leu	Val	Asn	Pro	Glu	Gly	Gln	Val	Val	Lys	Phe
				170					175					180
Trp	Arg	Pro	Glu	Glu	Pro	Ile	Glu	Val	Ile	Arg	Pro	Asp	Ile	Ala
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Ala	Leu	Val	Arg	Gln	Val	Ile	Ile	Lys	Lys	Lys	Glu	Asp	Leu	
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<210> 30
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 30
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<210> 31
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 31
gtatcttgtc aaccctgagg 20

<210> 32
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 32
taaccagagc tgctatgtca ggcc 24

<210> 33

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<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 33
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<210> 34
<211> 3721
<212> DNA
<213> Homo Sapien

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<210> 35

<211> 888

<212> PRT

<213> Homo Sapien

<400> 35

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				20					25					30	
Pro	Pro	Pro	Leu	Ser	Val	Ala	Pro	Arg	Asp	Tyr	Leu	Asn	His	Tyr	
				35					40					45	
Pro	Val	Phe	Val	Gly	Ser	Gly	Pro	Gly	Arg	Leu	Thr	Pro	Ala	Glu	
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Gly	Ala	Asp	Asp	Leu	Asn	Ile	Gln	Arg	Val	Leu	Arg	Val	Asn	Arg	
				65					70					75	
Thr	Leu	Phe	Ile	Gly	Asp	Arg	Asp	Asn	Leu	Tyr	Arg	Val	Glu	Leu	
				80					85					90	
Glu	Pro	Pro	Thr	Ser	Thr	Glu	Leu	Arg	Tyr	Gln	Arg	Lys	Leu	Thr	
				95					100					105	
Trp	Arg	Ser	Asn	Pro	Ser	Asp	Ile	Asn	Val	Cys	Arg	Met	Lys	Gly	
				110					115					120	
Lys	Gln	Glu	Gly	Glu	Cys	Arg	Asn	Phe	Val	Lys	Val	Leu	Leu	Leu	
				125					130					135	
Arg	Asp	Glu	Ser	Thr	Leu	Phe	Val	Cys	Gly	Ser	Asn	Ala	Phe	Asn	
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Pro	Val	Cys	Ala	Asn	Tyr	Ser	Ile	Asp	Thr	Leu	Gln	Pro	Val	Gly	
				155					160					165	
Asp	Asn	Ile	Ser	Gly	Met	Ala	Arg	Cys	Pro	Tyr	Asp	Pro	Lys	His	
				170					175					180	
Ala	Asn	Val	Ala	Leu	Phe	Ser	Asp	Gly	Met	Leu	Phe	Thr	Ala	Thr	
				185					190					195	
Val	Thr	Asp	Phe	Leu	Ala	Ile	Asp	Ala	Val	Ile	Tyr	Arg	Ser	Leu	
				200					205					210	
Gly	Asp	Arg	Pro	Thr	Leu	Arg	Thr	Val	Lys	His	Asp	Ser	Lys	Trp	
				215					220					225	
Phe	Lys	Glu	Pro	Tyr	Phe	Val	His	Ala	Val	Glu	Trp	Gly	Ser	His	
				230					235					240	
Val	Tyr	Phe	Phe	Phe	Arg	Glu	Ile	Ala	Met	Glu	Phe	Asn	Tyr	Leu	
				245					250					255	
Glu	Lys	Val	Val	Val	Ser	Arg	Val	Ala	Arg	Val	Cys	Lys	Asn	Asp	
				260					265					270	
Val	Gly	Gly	Ser	Pro	Arg	Val	Leu	Glu	Lys	Gln	Trp	Thr	Ser	Phe	
				275					280					285	
Leu	Lys	Ala	Arg	Leu	Asn	Cys	Ser	Val	Pro	Gly	Asp	Ser	His	Phe	
				290					295					300	
Tyr	Phe	Asn	Val	Leu	Gln	Ala	Val	Thr	Gly	Val	Val	Ser	Leu	Gly	

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Gly Arg Pro Val	Val Leu Ala Val Phe	Ser Thr Pro Ser Asn Ser			
	320	325			330
Ile Pro Gly Ser	Ala Val Cys Ala Phe	Asp Leu Thr Gln Val Ala			
	335	340			345
Ala Val Phe Glu	Gly Arg Phe Arg Glu	Gln Lys Ser Pro Glu Ser			
	350	355			360
Ile Trp Thr Pro	Val Pro Glu Asp Gln	Val Pro Arg Pro Arg Pro			
	365	370			375
Gly Cys Cys Ala	Ala Pro Gly Met Gln	Tyr Asn Ala Ser Ser Ala			
	380	385			390
Leu Pro Asp Asp	Ile Leu Asn Phe Val	Lys Thr His Pro Leu Met			
	395	400			405
Asp Glu Ala Val	Pro Ser Leu Gly His	Ala Pro Trp Ile Leu Arg			
	410	415			420
Thr Leu Met Arg	His Gln Leu Thr Arg	Val Ala Val Asp Val Gly			
	425	430			435
Ala Gly Pro Trp	Gly Asn Gln Thr Val	Val Phe Leu Gly Ser Glu			
	440	445			450
Ala Gly Thr Val	Leu Lys Phe Leu Val	Arg Pro Asn Ala Ser Thr			
	455	460			465
Ser Gly Thr Ser	Gly Leu Ser Val Phe	Leu Glu Glu Phe Glu Thr			
	470	475			480
Tyr Arg Pro Asp	Arg Cys Gly Arg Pro	Gly Gly Gly Glu Thr Gly			
	485	490			495
Gln Arg Leu Leu	Ser Leu Glu Leu Asp	Ala Ala Ser Gly Gly Leu			
	500	505			510
Leu Ala Ala Phe	Pro Arg Cys Val Val	Arg Val Pro Val Ala Arg			
	515	520			525
Cys Gln Gln Tyr	Ser Gly Cys Met Lys	Asn Cys Ile Gly Ser Gln			
	530	535			540
Asp Pro Tyr Cys	Gly Trp Ala Pro Asp	Gly Ser Cys Ile Phe Leu			
	545	550			555
Ser Pro Gly Thr	Arg Ala Ala Phe Glu	Gln Asp Val Ser Gly Ala			
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Ser Thr Ser Gly	Leu Gly Asp Cys Thr	Gly Leu Leu Arg Ala Ser			
	575	580			585
Leu Ser Glu Asp	Arg Ala Gly Leu Val	Ser Val Asn Leu Leu Val			
	590	595			600

Thr Ser Ser Val	Ala Ala Phe Val Val	Gly Ala Val Val Ser Gly	605	610	615
Phe Ser Val Gly	Trp Phe Val Gly Leu	Arg Glu Arg Arg Glu Leu	620	625	630
Ala Arg Arg Lys	Asp Lys Glu Ala Ile	Leu Ala His Gly Ala Gly	635	640	645
Glu Ala Val Leu	Ser Val Ser Arg Leu	Gly Glu Arg Arg Ala Gln	650	655	660
Gly Pro Gly Gly	Arg Gly Gly Gly Gly	Gly Gly Gly Ala Gly Val	665	670	675
Pro Pro Glu Ala	Leu Leu Ala Pro Leu	Met Gln Asn Gly Trp Ala	680	685	690
Lys Ala Thr Leu	Leu Gln Gly Gly Pro	His Asp Leu Asp Ser Gly	695	700	705
Leu Leu Pro Thr	Pro Glu Gln Thr Pro	Leu Pro Gln Lys Arg Leu	710	715	720
Pro Thr Pro His	Pro His Pro His Ala	Leu Gly Pro Arg Ala Trp	725	730	735
Asp His Gly His	Pro Leu Leu Pro Ala	Ser Ala Ser Ser Ser Leu	740	745	750
Leu Leu Leu Ala	Pro Ala Arg Ala Pro	Glu Gln Pro Pro Ala Pro	755	760	765
Gly Glu Pro Thr	Pro Asp Gly Arg Leu	Tyr Ala Ala Arg Pro Gly	770	775	780
Arg Ala Ser His	Gly Asp Phe Pro Leu	Thr Pro His Ala Ser Pro	785	790	795
Asp Arg Arg Arg	Val Val Ser Ala Pro	Thr Gly Pro Leu Asp Pro	800	805	810
Ala Ser Ala Ala	Asp Gly Leu Pro Arg	Pro Trp Ser Pro Pro Pro	815	820	825
Thr Gly Ser Leu	Arg Arg Pro Leu Gly	Pro His Ala Pro Pro Ala	830	835	840
Ala Thr Leu Arg	Arg Thr His Thr Phe	Asn Ser Gly Glu Ala Arg	845	850	855
Pro Gly Asp Arg	His Arg Gly Cys His	Ala Arg Pro Gly Thr Asp	860	865	870
Leu Ala His Leu	Leu Pro Tyr Gly Gly	Ala Asp Arg Thr Ala Pro	875	880	885
Pro Val Pro					

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<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 36
gaggacctac cggccggaca g 21

<210> 37
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 37
atacaccgcc agtactgctg gcag 24

<210> 38
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 38
agacagggca gcggtgctg agcttggagc tggacgcagc tt 42

<210> 39
<211> 2014
<212> DNA
<213> Homo Sapien

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<210> 40
 <211> 502
 <212> PRT
 <213> Homo Sapien

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 35 40 45
 Pro Ala Arg Tyr Phe Tyr Ile Gln Ala Val Asp Thr Ser Gly Asn
 50 55 60
 Lys Phe Thr Ser Ser Pro Gly Glu Lys Val Phe Gln Val Lys Val
 65 70 75
 Ser Ala Pro Glu Glu Gln Phe Thr Arg Val Gly Val Gln Val Leu
 80 85 90
 Asp Arg Lys Asp Gly Ser Phe Ile Val Arg Tyr Arg Met Tyr Ala
 95 100 105
 Ser Tyr Lys Asn Leu Lys Val Glu Ile Lys Phe Gln Gly Gln His
 110 115 120
 Val Ala Lys Ser Pro Tyr Ile Leu Lys Gly Pro Val Tyr His Glu
 125 130 135
 Asn Cys Asp Cys Pro Leu Gln Asp Ser Ala Ala Trp Leu Arg Glu
 140 145 150
 Met Asn Cys Pro Glu Thr Ile Ala Gln Ile Gln Arg Asp Leu Ala
 155 160 165
 His Phe Pro Ala Val Asp Pro Glu Lys Ile Ala Val Glu Ile Pro
 170 175 180
 Lys Arg Phe Gly Gln Arg Gln Ser Leu Cys His Tyr Thr Leu Lys
 185 190 195
 Asp Asn Lys Val Tyr Ile Lys Thr His Gly Glu His Val Gly Phe
 200 205 210
 Arg Ile Phe Met Asp Ala Ile Leu Leu Ser Leu Thr Arg Lys Val
 215 220 225
 Lys Met Pro Asp Val Glu Leu Phe Val Asn Leu Gly Asp Trp Pro

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Leu Glu Lys Lys	Lys Ser Asn Ser Asn	Ile His Pro Ile Phe Ser			
	245	250		255	
Trp Cys Gly Ser	Thr Asp Ser Lys Asp	Ile Val Met Pro Thr Tyr			
	260	265		270	
Asp Leu Thr Asp	Ser Val Leu Glu Thr	Met Gly Arg Val Ser Leu			
	275	280		285	
Asp Met Met Ser	Val Gln Ala Asn Thr	Gly Pro Pro Trp Glu Ser			
	290	295		300	
Lys Asn Ser Thr	Ala Val Trp Arg Gly	Arg Asp Ser Arg Lys Glu			
	305	310		315	
Arg Leu Glu Leu	Val Lys Leu Ser Arg	Lys His Pro Glu Leu Ile			
	320	325		330	
Asp Ala Ala Phe	Thr Asn Phe Phe Phe	Phe Lys His Asp Glu Asn			
	335	340		345	
Leu Tyr Gly Pro	Ile Val Lys His Ile	Ser Phe Phe Asp Phe Phe			
	350	355		360	
Lys His Lys Tyr	Gln Ile Asn Ile Asp	Gly Thr Val Ala Ala Tyr			
	365	370		375	
Arg Leu Pro Tyr	Leu Leu Val Gly Asp	Ser Val Val Leu Lys Gln			
	380	385		390	
Asp Ser Ile Tyr	Tyr Glu His Phe Tyr	Asn Glu Leu Gln Pro Trp			
	395	400		405	
Lys His Tyr Ile	Pro Val Lys Ser Asn	Leu Ser Asp Leu Leu Glu			
	410	415		420	
Lys Leu Lys Trp	Ala Lys Asp His Asp	Glu Glu Ala Lys Lys Ile			
	425	430		435	
Ala Lys Ala Gly	Gln Glu Phe Ala Arg	Asn Asn Leu Met Gly Asp			
	440	445		450	
Asp Ile Phe Cys	Tyr Tyr Phe Lys Leu	Phe Gln Glu Tyr Ala Asn			
	455	460		465	
Leu Gln Val Ser	Glu Pro Gln Ile Arg	Glu Gly Met Lys Arg Val			
	470	475		480	
Glu Pro Gln Thr	Glu Asp Asp Leu Phe	Pro Cys Thr Cys His Arg			
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Lys Lys Thr Lys	Asp Glu Leu				
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<211> 26

<212> DNA
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 42
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<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 42
cgataagctg ctacagtgcc atcg 24

<210> 43
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 43
gtgactgtcc tctgcaagat agtgcagcct ggctacggga 40

<210> 44
<211> 2395
<212> DNA
<213> Homo Sapien

<400> 44
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 ggatcaaggg acccactgca gtggcagcag gactgttggg cccccacccc 2150
 aaccctgcac agccctcatc cctctttggc ttgagccgtc agaggccctg 2200
 tgctgagtgt ctgaccgaga cactcacagc tttgtcatca gggcacaggc 2250
 ttctctggag ccaggatgat ctgtgccacg cttgcacctc gggcccatct 2300
 gggctcatgc tctctctcct gctattgaat tagtacctag ctgcacacag 2350
 tatgtagtta ccaaagaat aaacggcaat aattgagaaa aaaaa 2395

<210> 45
 <211> 310
 <212> PRT
 <213> Homo Sapien

<400> 45
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 Glu Val Leu Gly Ile Ala Val Phe Leu Arg Gly Phe Phe Pro Ala
 20 25 30
 Pro Val Arg Ser Ser Ala Arg Ala Glu His Gly Ala Glu Pro Pro
 35 40 45
 Ala Pro Glu Pro Ser Ala Gly Ala Ser Ser Asn Trp Thr Thr Leu
 50 55 60
 Pro Pro Pro Leu Phe Ser Lys Val Val Ile Val Leu Ile Asp Ala
 65 70 75
 Leu Arg Asp Asp Phe Val Phe Gly Ser Lys Gly Val Lys Phe Met
 80 85 90
 Pro Tyr Thr Thr Tyr Leu Val Glu Lys Gly Ala Ser His Ser Phe
 95 100 105
 Val Ala Glu Ala Lys Pro Pro Thr Val Thr Met Pro Arg Ile Lys
 110 115 120
 Ala Leu Met Thr Gly Ser Leu Pro Gly Phe Val Asp Val Ile Arg
 125 130 135
 Asn Leu Asn Ser Pro Ala Leu Leu Glu Asp Ser Val Ile Arg Gln
 140 145 150
 Ala Lys Ala Ala Gly Lys Arg Ile Val Phe Tyr Gly Asp Glu Thr
 155 160 165
 Trp Val Lys Leu Phe Pro Lys His Phe Val Glu Tyr Asp Gly Thr
 170 175 180

Thr	Ser	Phe	Phe	Val	Ser	Asp	Tyr	Thr	Glu	Val	Asp	Asn	Asn	Val
				185					190					195
Thr	Arg	His	Leu	Asp	Lys	Val	Leu	Lys	Arg	Gly	Asp	Trp	Asp	Ile
				200					205					210
Leu	Ile	Leu	His	Tyr	Leu	Gly	Leu	Asp	His	Ile	Gly	His	Ile	Ser
				215					220					225
Gly	Pro	Asn	Ser	Pro	Leu	Ile	Gly	Gln	Lys	Leu	Ser	Glu	Met	Asp
				230					235					240
Ser	Val	Leu	Met	Lys	Ile	His	Thr	Ser	Leu	Gln	Ser	Lys	Glu	Arg
				245					250					255
Glu	Thr	Pro	Leu	Pro	Asn	Leu	Leu	Val	Leu	Cys	Gly	Asp	His	Gly
				260					265					270
Met	Ser	Glu	Thr	Gly	Ser	His	Gly	Ala	Ser	Ser	Thr	Glu	Glu	Val
				275					280					285
Asn	Thr	Pro	Leu	Ile	Leu	Ile	Ser	Ser	Ala	Phe	Glu	Arg	Lys	Pro
				290					295					300
Gly	Asp	Ile	Arg	His	Pro	Lys	His	Val	Gln					
				305					310					

<210> 46
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 46
 cgggactttc gctacctgtt gc 22

 <210> 47
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 47
 catcatattc cacaaaatgc tttggg 26

 <210> 48
 <211> 38
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 48

ccttcgggga ttcttcccgg ctcccgttcg ttctcttg 38

<210> 49
<211> 918
<212> DNA
<213> Homo Sapien

<400> 49
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agcaatggca atgggggtcc ccagagtcac tctgctctgc ctctttgggg 100
ctgcgctctg cctgacaggg tcccaagccc tgcagtgcta cagctttgag 150
cacacctact ttggcccctt tgacctcagg gccatgaagc tgcccagcat 200
ctctgtctct catgagtgtt ttgaggctat cctgtctctg gacaccgggt 250
atcgcgcgcc ggtgaccctg gtgcggaagg gctgctggac cgggcctcct 300
gcggggccaga cgcaatcgaa cccggacgcg ctgccgccag actactcggg 350
ggtgcgcgcc tgcaacaactg acaaatgcaa cgcccacctc atgactcatg 400
acgccctccc caacctgagc caagcaccgc acccgccgac gctcagcggc 450
gccgagtgtt acgcctgtat cgggggtccac caggatgact gcgctatcgg 500
caggtcccga cgagtccagt gtcaccagga ccagaccgcc tgcttccagg 550
gcagtggcag aatgacagtt ggcaatttct cagtccctgt gtacatcaga 600
acctgccacc ggccctcctg caccaccgag ggaccacca gccctggac 650
agccatcgac ctccaggggt cctgctgtga ggggtacctc tgcaacagga 700
aatccatgac ccagcccttc accagtgtt cagccaccac ccctccccga 750
gcactacagg tcctggccct gtcctccca gtcctcctgc tgggtggggct 800
ctcagcatag accgcccctc caggatgttg gggacagggc tcacacacct 850
cattcttgct gcttcagccc ctatcacata gctcactgga aaatgatgtt 900
aaagtaagaa ttgcaaaa 918

<210> 50
<211> 251
<212> PRT
<213> Homo Sapien

<400> 50
Met Ala Met Gly Val Pro Arg Val Ile Leu Leu Cys Leu Phe Gly
1 5 10 15
Ala Ala Leu Cys Leu Thr Gly Ser Gln Ala Leu Gln Cys Tyr Ser
20 25 30

Phe	Glu	His	Thr	Tyr	Phe	Gly	Pro	Phe	Asp	Leu	Arg	Ala	Met	Lys	35	40	45
Leu	Pro	Ser	Ile	Ser	Cys	Pro	His	Glu	Cys	Phe	Glu	Ala	Ile	Leu	50	55	60
Ser	Leu	Asp	Thr	Gly	Tyr	Arg	Ala	Pro	Val	Thr	Leu	Val	Arg	Lys	65	70	75
Gly	Cys	Trp	Thr	Gly	Pro	Pro	Ala	Gly	Gln	Thr	Gln	Ser	Asn	Pro	80	85	90
Asp	Ala	Leu	Pro	Pro	Asp	Tyr	Ser	Val	Val	Arg	Gly	Cys	Thr	Thr	95	100	105
Asp	Lys	Cys	Asn	Ala	His	Leu	Met	Thr	His	Asp	Ala	Leu	Pro	Asn	110	115	120
Leu	Ser	Gln	Ala	Pro	Asp	Pro	Pro	Thr	Leu	Ser	Gly	Ala	Glu	Cys	125	130	135
Tyr	Ala	Cys	Ile	Gly	Val	His	Gln	Asp	Asp	Cys	Ala	Ile	Gly	Arg	140	145	150
Ser	Arg	Arg	Val	Gln	Cys	His	Gln	Asp	Gln	Thr	Ala	Cys	Phe	Gln	155	160	165
Gly	Ser	Gly	Arg	Met	Thr	Val	Gly	Asn	Phe	Ser	Val	Pro	Val	Tyr	170	175	180
Ile	Arg	Thr	Cys	His	Arg	Pro	Ser	Cys	Thr	Thr	Glu	Gly	Thr	Thr	185	190	195
Ser	Pro	Trp	Thr	Ala	Ile	Asp	Leu	Gln	Gly	Ser	Cys	Cys	Glu	Gly	200	205	210
Tyr	Leu	Cys	Asn	Arg	Lys	Ser	Met	Thr	Gln	Pro	Phe	Thr	Ser	Ala	215	220	225
Ser	Ala	Thr	Thr	Pro	Pro	Arg	Ala	Leu	Gln	Val	Leu	Ala	Leu	Leu	230	235	240
Leu	Pro	Val	Leu	Leu	Leu	Val	Gly	Leu	Ser	Ala					245	250	

<210> 51

<211> 3288

<212> DNA

<213> Homo Sapien

<400> 51

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gattgggaaa gggaaaggac aaaaaagacc cctgggctac acggcgtagg 100

tgcagggttt cctactgctg ttcttttatg ctgggagctg tggctgtaac 150

caactaggaa ataacgtatg cagcagctat ggctgtcaga gagttgtgct 200

tcccaagaca aaggcaagtc ctgtttcttt ttcttttttg gggagtgtcc 250
 ttggcagggt ctgggttttg acgttattcg gtgactgagg aaacagagaa 300
 aggatccttt gtggtcaatc tggcaaagga tctgggacta gcagaggggg 350
 agctggctgc aaggggaacc aggggtggtt ccgatgataa caaacaatac 400
 ctgctcctgg attcacatac cgggaatttg ctcaaaatg agaaactgga 450
 ccgagagaag ctgtgtggcc ctaaagagcc ctgtatgctg tatttccaaa 500
 ttttaatgga tgatcccttt cagatttacc gggctgagct gagagtcagg 550
 gatataaatg atcacgcgcc agtatttcag gacaaagaaa cagtcttaaa 600
 aatatcagaa aatacagctg aaggacagc atttagacta gaaagagcac 650
 aggatccaga tggaggactt aacggtatcc aaaactacac gatcagcccc 700
 aactcttttt tccatattaa cattagtggc ggtgatgaag gcatgatata 750
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 tcagcttaac cctcacagcg ctggatggtg ggtctccatc caggctctggg 850
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 cctactaaaa ctttctgttg agaattttta catcctaatt acagaaggcg 1400
 cgctggacag agagatcaga gccgagtaca acatcactat caccgtcact 1450
 gacttgggga caccaggtt gaaaaccgag cacaacataa cggctcctgg 1500
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 tgttcgccg cgagaacaac agccccgcc tgcacatcgg cagcgtcagc 1600
 gccacagaca gagactcggg caccaacgcc caggtcacct actcgtgct 1650

ccttagttta tataacttatt attttatctt taagcatgct acttttactt 3150
 ggccaatatt ttcttatggt aacttttgct gatgtataaa acagactatg 3200
 ccttataatt gaaataaaat tataatctgc ctgaaaatga ataaaaataa 3250
 aacattttga aatgtgaaaa aaaaaaaaaa aaaaaaaaaa 3288

<210> 52
 <211> 800
 <212> PRT
 <213> Homo Sapien

<400> 52
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 20 25 30
 Gly Arg Tyr Ser Val Thr Glu Glu Thr Glu Lys Gly Ser Phe Val
 35 40 45
 Val Asn Leu Ala Lys Asp Leu Gly Leu Ala Glu Gly Glu Leu Ala
 50 55 60
 Ala Arg Gly Thr Arg Val Val Ser Asp Asp Asn Lys Gln Tyr Leu
 65 70 75
 Leu Leu Asp Ser His Thr Gly Asn Leu Leu Thr Asn Glu Lys Leu
 80 85 90
 Asp Arg Glu Lys Leu Cys Gly Pro Lys Glu Pro Cys Met Leu Tyr
 95 100 105
 Phe Gln Ile Leu Met Asp Asp Pro Phe Gln Ile Tyr Arg Ala Glu
 110 115 120
 Leu Arg Val Arg Asp Ile Asn Asp His Ala Pro Val Phe Gln Asp
 125 130 135
 Lys Glu Thr Val Leu Lys Ile Ser Glu Asn Thr Ala Glu Gly Thr
 140 145 150
 Ala Phe Arg Leu Glu Arg Ala Gln Asp Pro Asp Gly Gly Leu Asn
 155 160 165
 Gly Ile Gln Asn Tyr Thr Ile Ser Pro Asn Ser Phe Phe His Ile
 170 175 180
 Asn Ile Ser Gly Gly Asp Glu Gly Met Ile Tyr Pro Glu Leu Val
 185 190 195
 Leu Asp Lys Ala Leu Asp Arg Glu Glu Gln Gly Glu Leu Ser Leu
 200 205 210
 Thr Leu Thr Ala Leu Asp Gly Gly Ser Pro Ser Arg Ser Gly Thr
 215 220 225

Ser Thr Val Arg	Ile Val Val Leu Asp	Val Asn Asp Asn Ala Pro	230	235	240
Gln Phe Ala Gln	Ala Leu Tyr Glu Thr	Gln Ala Pro Glu Asn Ser	245	250	255
Pro Ile Gly Phe	Leu Ile Val Lys Val	Trp Ala Glu Asp Val Asp	260	265	270
Ser Gly Val Asn	Ala Glu Val Ser Tyr	Ser Phe Phe Asp Ala Ser	275	280	285
Glu Asn Ile Arg	Thr Thr Phe Gln Ile	Asn Pro Phe Ser Gly Glu	290	295	300
Ile Phe Leu Arg	Glu Leu Leu Asp Tyr	Glu Leu Val Asn Ser Tyr	305	310	315
Lys Ile Asn Ile	Gln Ala Met Asp Gly	Gly Gly Leu Ser Ala Arg	320	325	330
Cys Arg Val Leu	Val Glu Val Leu Asp	Thr Asn Asp Asn Pro Pro	335	340	345
Glu Leu Ile Val	Ser Ser Phe Ser Asn	Ser Val Ala Glu Asn Ser	350	355	360
Pro Glu Thr Pro	Leu Ala Val Phe Lys	Ile Asn Asp Arg Asp Ser	365	370	375
Gly Glu Asn Gly	Lys Met Val Cys Tyr	Ile Gln Glu Asn Leu Pro	380	385	390
Phe Leu Leu Lys	Pro Ser Val Glu Asn	Phe Tyr Ile Leu Ile Thr	395	400	405
Glu Gly Ala Leu	Asp Arg Glu Ile Arg	Ala Glu Tyr Asn Ile Thr	410	415	420
Ile Thr Val Thr	Asp Leu Gly Thr Pro	Arg Leu Lys Thr Glu His	425	430	435
Asn Ile Thr Val	Leu Val Ser Asp Val	Asn Asp Asn Ala Pro Ala	440	445	450
Phe Thr Gln Thr	Ser Tyr Thr Leu Phe	Val Arg Glu Asn Asn Ser	455	460	465
Pro Ala Leu His	Ile Gly Ser Val Ser	Ala Thr Asp Arg Asp Ser	470	475	480
Gly Thr Asn Ala	Gln Val Thr Tyr Ser	Leu Leu Pro Pro Gln Asp	485	490	495
Pro His Leu Pro	Leu Ala Ser Leu Val	Ser Ile Asn Ala Asp Asn	500	505	510
Gly His Leu Phe	Ala Leu Arg Ser Leu	Asp Tyr Glu Ala Leu Gln			

	515		520		525
Ala Phe Glu Phe	Arg Val Gly Ala Thr	Asp Arg Gly Ser Pro	Ala		
	530	535	540		
Leu Ser Arg Glu	Ala Leu Val Arg Val	Leu Val Leu Asp Ala	Asn		
	545	550	555		
Asp Asn Ser Pro	Phe Val Leu Tyr Pro	Leu Gln Asn Gly Ser	Ala		
	560	565	570		
Pro Cys Thr Glu	Leu Val Pro Arg Ala	Ala Glu Pro Gly Tyr	Leu		
	575	580	585		
Val Thr Lys Val	Val Ala Val Asp Gly	Asp Ser Gly Gln Asn	Ala		
	590	595	600		
Trp Leu Ser Tyr	Gln Leu Leu Lys Ala	Thr Glu Pro Gly Leu	Phe		
	605	610	615		
Gly Val Trp Ala	His Asn Gly Glu Val	Arg Thr Ala Arg Leu	Leu		
	620	625	630		
Ser Glu Arg Asp	Ala Ala Lys His Arg	Leu Val Val Leu Val	Lys		
	635	640	645		
Asp Asn Gly Glu	Pro Pro Arg Ser Ala	Thr Ala Thr Leu His	Leu		
	650	655	660		
Leu Leu Val Asp	Gly Phe Ser Gln Pro	Tyr Leu Pro Leu Pro	Glu		
	665	670	675		
Ala Ala Pro Ala	Gln Ala Gln Ala Glu	Ala Asp Leu Leu Thr	Val		
	680	685	690		
Tyr Leu Val Val	Ala Leu Ala Ser Val	Ser Ser Leu Phe Leu	Leu		
	695	700	705		
Ser Val Leu Leu	Phe Val Ala Val Arg	Leu Cys Arg Arg Ser	Arg		
	710	715	720		
Ala Ala Ser Val	Gly Arg Cys Ser Val	Pro Glu Gly Pro Phe	Pro		
	725	730	735		
Gly His Leu Val	Asp Val Arg Gly Ala	Glu Thr Leu Ser Gln	Ser		
	740	745	750		
Tyr Gln Tyr Glu	Val Cys Leu Thr Gly	Gly Pro Gly Thr Ser	Glu		
	755	760	765		
Phe Lys Phe Leu	Lys Pro Val Ile Ser	Asp Ile Gln Ala Gln	Gly		
	770	775	780		
Pro Gly Arg Lys	Gly Glu Glu Asn Ser	Thr Phe Arg Asn Ser	Phe		
	785	790	795		
Gly Phe Asn Ile	Gln				
	800				

<210> 53
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 53
ctggggagtg tccttggcag gttc 24

<210> 54
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 54
cagcatagag ggctcttttag ggcacac 27

<210> 55
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 55
cggtgactga ggaaacagag aaaggatcct ttgtggtcaa tctggc 46

<210> 56
<211> 2242
<212> DNA
<213> Homo Sapien

<220>
<221> unsure
<222> 2181
<223> unknown base

<400> 56
gaatgaatac ctccgaagcc gctttgttct ccagatgtga atagctccac 50
tataccagcc tcgtcttctt tccgggggac aacgtgggtc agggcacaga 100
gagatattta atgtcaccct cttgggggctt tcatgggact ccctctgcca 150
catttttttg aggttgggaa agttgctaga ggcttcagaa ctccagccta 200
atggatccca aactcgggag aatggctgcg tccctgctgg ctgtgctgct 250
gctgctgctg gagcgcgga tggtctctc accctccccg cccccggcgc 300
tgtagagaa agtcttccag tacattgacc tccatcagga tgaatttgtg 350

cagacgctga aggagtgggt ggccatcgag agcgactctg tccagcctgt 400
 gcctcgcttc agacaagagc tcttcagaat gatggccgtg gctgoggaca 450
 cgctgcagcg cctggggggc cgtgtggcct cgggtggacat gggtcctcag 500
 cagctgcccg atggtcagag tcttccaata cctcccgtca tcttgccga 550
 actggggagc gatcccacga aaggcaccgt gtgcttctac ggccacttgg 600
 acgtgcagcc tgctgaccgg ggcgatgggt ggctcacgga cccctatgtg 650
 ctgacggagg tagacgggaa actttatgga cgaggagcga ccgacaacaa 700
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 agcaagatct tctgtgaat atcaaattca tcattgaggg gatggaagag 800
 gctggctctg ttgccctgga ggaacttgtg gaaaaagaaa aggaccgatt 850
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 aaaggaagcc agcaatcact tatggaaccc gggggaacag ctacttcatg 950
 gtggaggtga aatgcagaga ccaggatttt cactcaggaa cctttggtgg 1000
 catccttcat gaaccaatgg ctgatctgggt tgctcttctc ggtagcctgg 1050
 tagactcgtc tggatcatatc ctgggtccctg gaatctatga tgaagtgggt 1100
 cctcttacag aagaggaaat aaatacatatc aaagccatcc atctagacct 1150
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 aggaggagat tctaatgcac ctctggaggt acccatctct ttctattcat 1250
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 ccgagttata ggaaaatttt caatccgtct agtccctcac atgaatgtgt 1350
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 agaaatagtt ccaacaagat ggttgtttcc atgactctag gactacaccc 1450
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aaatatccag agaatttggg tctagtatag tacattttcc cttccattta 1850
 aaatgtcttg ggatatctgg atcagtaata aaatatttca aaggcacaga 1900
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 2242

<210> 57
 <211> 507
 <212> PRT
 <213> Homo Sapien

<400> 57

Met	Asp	Pro	Lys	Leu	Gly	Arg	Met	Ala	Ala	Ser	Leu	Leu	Ala	Val
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Leu	Leu	Leu	Leu	Leu	Glu	Arg	Gly	Met	Phe	Ser	Ser	Pro	Ser	Pro
				20					25					30
Pro	Pro	Ala	Leu	Leu	Glu	Lys	Val	Phe	Gln	Tyr	Ile	Asp	Leu	His
				35					40					45
Gln	Asp	Glu	Phe	Val	Gln	Thr	Leu	Lys	Glu	Trp	Val	Ala	Ile	Glu
				50					55					60
Ser	Asp	Ser	Val	Gln	Pro	Val	Pro	Arg	Phe	Arg	Gln	Glu	Leu	Phe
				65					70					75
Arg	Met	Met	Ala	Val	Ala	Ala	Asp	Thr	Leu	Gln	Arg	Leu	Gly	Ala
				80					85					90
Arg	Val	Ala	Ser	Val	Asp	Met	Gly	Pro	Gln	Gln	Leu	Pro	Asp	Gly
				95					100					105
Gln	Ser	Leu	Pro	Ile	Pro	Pro	Val	Ile	Leu	Ala	Glu	Leu	Gly	Ser
				110					115					120
Asp	Pro	Thr	Lys	Gly	Thr	Val	Cys	Phe	Tyr	Gly	His	Leu	Asp	Val
				125					130					135
Gln	Pro	Ala	Asp	Arg	Gly	Asp	Gly	Trp	Leu	Thr	Asp	Pro	Tyr	Val
				140					145					150
Leu	Thr	Glu	Val	Asp	Gly	Lys	Leu	Tyr	Gly	Arg	Gly	Ala	Thr	Asp
				155					160					165
Asn	Lys	Gly	Pro	Val	Leu	Ala	Trp	Ile	Asn	Ala	Val	Ser	Ala	Phe

Val Leu Ile Pro Leu Gly Ala Val Asp Asp Gly Glu His Ser Gln
470 480

Asn Glu Lys Ile Asn Arg Trp Asn Tyr Ile Glu Gly Thr Lys Leu
485 490 495

Phe Ala Ala Phe Phe Leu Glu Met Ala Gln Leu His
500 505

<210> 58
<211> 1470
<212> DNA
<213> Homo Sapien

<400> 58
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ctttgtcatg ggacctgtgc gggtgggaat attgcttttc ctttttttg 150
ccgtgcacga ggcttgggct gggatgttga aggaggagga cgatgacaca 200
gaacgcttgc ccagcaaagtg cgaagtgtgt aagctgctga gcacagagct 250
acaggcggaa ctgagtcgca ccggtcgac tcgagaggtg ctggagctgg 300
ggcaggtgct ggatacagc aagaggaaga gacacgtgcc ttacagcgtt 350
tcagagacaa ggctggaaga ggccttagag aatttatgtg agcggatcct 400
ggactatagt gttcacgtg agcgcaagg ctcactgaga tatgccaagg 450
gtcagagtca gaccatggca aactgaaag gcctagtga gaaggggtg 500
aaggtggatc tggggatccc tctggagctt tgggatgagc ccagcgtgga 550
ggtcacatac ctcaagaagc agtgtgagac catgttgag gagtttgaag 600
acattgtggg agactggtac ttccaccatc aggagcagcc cctacaaaat 650
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ggaaacttgg actggaaagg agatcacaga tggggaagag aaaacagaag 750
gggaggaaga gcaggaggag gaggaggaag aggaggaaga ggaaggggga 800
gacaagatga ccaagacagg aagccacccc aaacttgacc gagaagatct 850
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tctaaagcct gactctccc tgctccacag ctttcagggt gtgtttatga 950
gtgactccac ccaagcttgt agctgttctc tccatctaa cctcaggcaa 1000
gatcctgggtg aaacagcatg acatggcttc tggggtggag ggtgggggtg 1050
gaggtcctgc tcctagagat gaactctatc cagcccctta attggcaggt 1100

gtatgtgctg acagtactga aagctttcct cttaaactga tcccaccccc 1150
 acccaaaagt cagcagtggc actggagctg tgggctttgg ggaagtcact 1200
 tagctcctta aggtctgttt ttagaccctt ccaaggaaga ggccagaacg 1250
 gacattctct gcgatctata tacattgcct gtatccagga ggctacacac 1300
 cagcaaaccg tgaaggagaa tgggacactg ggtcatggcc tggagttgct 1350
 gataatttag gtgggataga tacttggtct acttaagctc aatgtaaccc 1400
 agagcccacc atatatgttt ataggtgctc aactttctat atcgctatta 1450
 aacttttttc tttttttcta 1470

<210> 59
 <211> 248
 <212> PRT
 <213> Homo Sapien

<400> 59

Met	Gly	Pro	Val	Arg	Leu	Gly	Ile	Leu	Leu	Phe	Leu	Phe	Leu	Ala	1	5	10	15
Val	His	Glu	Ala	Trp	Ala	Gly	Met	Leu	Lys	Glu	Glu	Asp	Asp	Asp	20	25	30	
Thr	Glu	Arg	Leu	Pro	Ser	Lys	Cys	Glu	Val	Cys	Lys	Leu	Leu	Ser	35	40	45	
Thr	Glu	Leu	Gln	Ala	Glu	Leu	Ser	Arg	Thr	Gly	Arg	Ser	Arg	Glu	50	55	60	
Val	Leu	Glu	Leu	Gly	Gln	Val	Leu	Asp	Thr	Gly	Lys	Arg	Lys	Arg	65	70	75	
His	Val	Pro	Tyr	Ser	Val	Ser	Glu	Thr	Arg	Leu	Glu	Glu	Ala	Leu	80	85	90	
Glu	Asn	Leu	Cys	Glu	Arg	Ile	Leu	Asp	Tyr	Ser	Val	His	Ala	Glu	95	100	105	
Arg	Lys	Gly	Ser	Leu	Arg	Tyr	Ala	Lys	Gly	Gln	Ser	Gln	Thr	Met	110	115	120	
Ala	Thr	Leu	Lys	Gly	Leu	Val	Gln	Lys	Gly	Val	Lys	Val	Asp	Leu	125	130	135	
Gly	Ile	Pro	Leu	Glu	Leu	Trp	Asp	Glu	Pro	Ser	Val	Glu	Val	Thr	140	145	150	
Tyr	Leu	Lys	Lys	Gln	Cys	Glu	Thr	Met	Leu	Glu	Glu	Phe	Glu	Asp	155	160	165	
Ile	Val	Gly	Asp	Trp	Tyr	Phe	His	His	Gln	Glu	Gln	Pro	Leu	Gln	170	175	180	

Asn Phe Leu Cys Glu Gly His Val Leu Pro Ala Ala Glu Thr Ala
 185 190 195
 Cys Leu Gln Glu Thr Trp Thr Gly Lys Glu Ile Thr Asp Gly Glu
 200 205 210
 Glu Lys Thr Glu Gly Glu Glu Glu Gln Glu Glu Glu Glu Glu
 215 220 225
 Glu Glu Glu Glu Gly Gly Asp Lys Met Thr Lys Thr Gly Ser His
 230 235 240
 Pro Lys Leu Asp Arg Glu Asp Leu
 245

<210> 60
 <211> 890
 <212> DNA
 <213> Homo Sapien

<400> 60
 aagtacttgt gtccgggtgg tggactggat tagctgcgga gccctggaag 50
 ctgcctgtcc ttctccctgt gcttaaccag aggtgcccat gggttggaca 100
 atgaggctgg tcacagcagc actgttactg ggtctcatga tggagggtcac 150
 tggagacgag gatgagaaca gcccggtgtgc ccatgaggcc ctcttggacg 200
 aggacaccct cttttgccag ggccttgaag ttttctaccc agagttgggg 250
 aacattggct gcaagggtgt tcctgattgt aacaactaca gacagaagat 300
 cacctcctgg atggagccga tagtcaagtt cccggggggcc gtggacggcg 350
 caacctatat cctgggtgatg gtggatccag atgcccctag cagagcagaa 400
 cccagacaga gattctggag acattggctg gtaacagata tcaagggcgc 450
 cgacctgaag aaaggaaga ttcagggcca ggagttatca gcctaccagg 500
 ctccctcccc accggcacac agtggccttc atcgctacca gttctttgtc 550
 tatcttcagg aaggaaaagt catctctctc cttccaagg aaaacaaaac 600
 tcgaggctct tggaaaatgg acagatttct gaaccgcttc cacctgggcg 650
 aacctgaagc aagcaccag ttcatgacct agaactacca ggactcacca 700
 accctccagg ctcccagagg aagggccagc gagccaagc acaaaaccag 750
 gcagagatag ctgcctgcta gatagccggc ttgcatcc gggcatgtgg 800
 ccacactgct caccaccgac gatgtgggta tggaaccccc tctggataca 850
 gaacccttc ttttccaaat taataaaaaa aatcatcaaa 890

<210> 61

<211> 223
 <212> PRT
 <213> Homo Sapien

<400> 61

Met	Gly	Trp	Thr	Met	Arg	Leu	Val	Thr	Ala	Ala	Leu	Leu	Leu	Gly	1	5	10	15
Leu	Met	Met	Val	Val	Thr	Gly	Asp	Glu	Asp	Glu	Asn	Ser	Pro	Cys	20	25	30	
Ala	His	Glu	Ala	Leu	Leu	Asp	Glu	Asp	Thr	Leu	Phe	Cys	Gln	Gly	35	40	45	
Leu	Glu	Val	Phe	Tyr	Pro	Glu	Leu	Gly	Asn	Ile	Gly	Cys	Lys	Val	50	55	60	
Val	Pro	Asp	Cys	Asn	Asn	Tyr	Arg	Gln	Lys	Ile	Thr	Ser	Trp	Met	65	70	75	
Glu	Pro	Ile	Val	Lys	Phe	Pro	Gly	Ala	Val	Asp	Gly	Ala	Thr	Tyr	80	85	90	
Ile	Leu	Val	Met	Val	Asp	Pro	Asp	Ala	Pro	Ser	Arg	Ala	Glu	Pro	95	100	105	
Arg	Gln	Arg	Phe	Trp	Arg	His	Trp	Leu	Val	Thr	Asp	Ile	Lys	Gly	110	115	120	
Ala	Asp	Leu	Lys	Lys	Gly	Lys	Ile	Gln	Gly	Gln	Glu	Leu	Ser	Ala	125	130	135	
Tyr	Gln	Ala	Pro	Ser	Pro	Pro	Ala	His	Ser	Gly	Phe	His	Arg	Tyr	140	145	150	
Gln	Phe	Phe	Val	Tyr	Leu	Gln	Glu	Gly	Lys	Val	Ile	Ser	Leu	Leu	155	160	165	
Pro	Lys	Glu	Asn	Lys	Thr	Arg	Gly	Ser	Trp	Lys	Met	Asp	Arg	Phe	170	175	180	
Leu	Asn	Arg	Phe	His	Leu	Gly	Glu	Pro	Glu	Ala	Ser	Thr	Gln	Phe	185	190	195	
Met	Thr	Gln	Asn	Tyr	Gln	Asp	Ser	Pro	Thr	Leu	Gln	Ala	Pro	Arg	200	205	210	
Gly	Arg	Ala	Ser	Glu	Pro	Lys	His	Lys	Thr	Arg	Gln	Arg	215	220				

<210> 62
 <211> 1321
 <212> DNA
 <213> Homo Sapien

<400> 62

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tgtagataaa gaccctttct tgccaggtgc tgagacaacc acactatgag 100
 aggcactcca ggagacgctg atggtggagg aagggccgtc tatcaatcaa 150
 tcaactgttg tgttatcaca tgcaagtatc cagaggctct tgagcaaggc 200
 agaggggata ccatttattt gggaatccag aatccagaaa tgtgtttgta 250
 ttgtgagaag gttggagaac agcccacatt gcagctaaaa gagcagaaga 300
 tcatggatct gtatggccaa cccgagcccc tgaaaccctt cttttctac 350
 cgtgccaaga ctggtaggac ctccaccctt gagtctgtgg ctttcccga 400
 ctggttcatt gcctcctcca agagagacca gccatcatt ctgacttcag 450
 aacttgggaa gtcatacaac actgcctttg aattaaatat aaatgactga 500
 actcagccta gaggtggcag cttggtcttt gtcttaaagt ttctggttcc 550
 caatgtgttt t'cgtctacat tttcttagtg tcattttcac gctggtgctg 600
 agacaggagc aaggctgctg ttatcatctc attttataat gaagaagaag 650
 caattacttc atagcaactg aagaacagga tgtggcctca gaagcaggag 700
 agctgggtgg tataaggctg tcctctcaag ctggtgctgt gtaggccaca 750
 aggcactctgc atgagtgact ttaagactca aagaccaaac actgagcttt 800
 cttctagggg tgggtatgaa gatgcttcag agctcatgcg cgttaccac 850
 gatggcatga ctagcacaga gctgatctct gtttctgttt tgctttattc 900
 cctcttggga tgatcatc cagtctttat atgttgccaa tatacctcat 950
 tgtgtgtaat agaacccttct tagcattaag accttgtaaa caaaaataat 1000
 tcttgggggtg ggtatgaaga tgcttcagag ctcatgcgcg ttaccacga 1050
 tggcatgact agcacagagc tgatctctgt ttctgttttg ctttattccc 1100
 tcttgggatg atatcatcca gtctttatat gttgccaata tacctcattg 1150
 tgtgtaatag aaccttctta gcattaagac cttgtaaaca aaaataattc 1200
 ttgtgttaag ttaaatacatt tttgtcctaa ttgtaatgtg taatcttaaa 1250
 gttaaataaa ctttgtgtat ttatataata ataaagctaa aactgatata 1300
 aaataaagaa agagtaaact g 1321

<210> 63
 <211> 134
 <212> PRT
 <213> Homo Sapien
 <400> 63

Met Arg Gly Thr Pro Gly Asp Ala Asp Gly Gly Gly Arg Ala Val
 1 5 10 15
 Tyr Gln Ser Ile Thr Val Ala Val Ile Thr Cys Lys Tyr Pro Glu
 20 25 30
 Ala Leu Glu Gln Gly Arg Gly Asp Pro Ile Tyr Leu Gly Ile Gln
 35 40 45
 Asn Pro Glu Met Cys Leu Tyr Cys Glu Lys Val Gly Glu Gln Pro
 50 55 60
 Thr Leu Gln Leu Lys Glu Gln Lys Ile Met Asp Leu Tyr Gly Gln
 65 70 75
 Pro Glu Pro Val Lys Pro Phe Leu Phe Tyr Arg Ala Lys Thr Gly
 80 85 90
 Arg Thr Ser Thr Leu Glu Ser Val Ala Phe Pro Asp Trp Phe Ile
 95 100 105
 Ala Ser Ser Lys Arg Asp Gln Pro Ile Ile Leu Thr Ser Glu Leu
 110 115 120
 Gly Lys Ser Tyr Asn Thr Ala Phe Glu Leu Asn Ile Asn Asp
 125 130

<210> 64
 <211> 999
 <212> DNA
 <213> Homo Sapien

<400> 64
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 gtgctgctgc tgctcctggc gggagccccc gccgcgcggc ccaactcccc 100
 gacctgtac tcccgcctgc gggccctgag ccaggagatc acccgcgact 150
 tcaacctcct gcaggtctcg gagccctcgg agccatgtgt gagatacctg 200
 cccaggctgt acctggacat acacaattac tgtgtgctgg acaagctgcg 250
 ggactttgtg gcctcgcccc cgtgttgga aagtgcccag gtagattcct 300
 tgaaggacaa agcacggaag ctgtacacca tcatgaactc gttctgcagg 350
 agagatttgg tattcctgtt ggatgactgc aatgccttgg aatacccaat 400
 cccagtgact acggtcctgc cagatcgtca gcgctaaggg aactgagacc 450
 agagaaagaa cccaagagaa ctaaagttat gtcagctacc cagacttaat 500
 gggccagagc catgaccctc acaggtcttg tgtagttgt atctgaaact 550
 gttatgtatc tctctacctt ctggaaaaca gggctggtat tcctaccag 600
 gaacctcctt tgagcataga gtagcaacc atgcttctca ttcccttgac 650

tcattgtcttg ccaggatggt tagatacaca gcatgttgat ttggtcacta 700
 aaaagaagaa aaggactaac aagcttcact tttatgaaca actatattga 750
 gaacatgcac aatagtatgt ttttattact ggtttaatgg agtaatggta 800
 cttttattct ttcttgatag aaacctgctt acatttaacc aagcttctat 850
 tatgcctttt tctaacacag actttcttca ctgtctttca tttaaaaaga 900
 aattaatgct ctttaagatat atattttacg tagtgctgac aggaccact 950
 ctttcattga aaggtgatga aaatcaaata aagaatctct tcacatgga 999

<210> 65
 <211> 136
 <212> PRT
 <213> Homo Sapien

<400> 65
 Met Arg Thr Pro Gly Pro Leu Pro Val Leu Leu Leu Leu Ala
 1 5 10 15
 Gly Ala Pro Ala Ala Arg Pro Thr Pro Pro Thr Cys Tyr Ser Arg
 20 25 30
 Met Arg Ala Leu Ser Gln Glu Ile Thr Arg Asp Phe Asn Leu Leu
 35 40 45
 Gln Val Ser Glu Pro Ser Glu Pro Cys Val Arg Tyr Leu Pro Arg
 50 55 60
 Leu Tyr Leu Asp Ile His Asn Tyr Cys Val Leu Asp Lys Leu Arg
 65 70 75
 Asp Phe Val Ala Ser Pro Pro Cys Trp Lys Val Ala Gln Val Asp
 80 85 90
 Ser Leu Lys Asp Lys Ala Arg Lys Leu Tyr Thr Ile Met Asn Ser
 95 100 105
 Phe Cys Arg Arg Asp Leu Val Phe Leu Leu Asp Asp Cys Asn Ala
 110 115 120
 Leu Glu Tyr Pro Ile Pro Val Thr Thr Val Leu Pro Asp Arg Gln
 125 130 135

Arg

<210> 66
 <211> 1893
 <212> DNA
 <213> Homo Sapien

<400> 66
 gtctccgcgt cacaggaact tcagcaccca cagggcggac agcgctcccc 50

tctacctgga gacttgactc ccgcgcgccc caaccctgct tatcccttga 100
ccgtcgagtg tcagagatcc tgcagccgcc cagtcccggc ccctctcccg 150
ccccacaccc accctcctgg ctcttcctgt ttttactcct ccttttcatt 200
cataacaaaa gctacagctc caggagccca gcgccgggct gtgacccaag 250
ccgagcgtgg aagaatgggg ttcttcggga ccggcacttg gattctggtg 300
ttagtgtcc cgattcaagc tttcccaaaa cctggaggaa gccaagacaa 350
atctctacat aatagagaat taagtgcaga aagacctttg aatgaacaga 400
ttgctgaagc agaagaagac aagattaaaa aaacatatcc tccagaaaac 450
aagccaggtc agagcaacta ttcttttgtt gataacttga acctgctaaa 500
ggcaataaca gaaaaggaaa aaattgagaa agaaagacaa tctataagaa 550
gctccccact tgataataag ttgaatgtgg aagatgttga ttcaaccaag 600
aatcgaaaac tgatcgatga ttatgactct actaagagtg gattggatca 650
taaatttcaa gatgatccag atggctcttca tcaactagac gggactcctt 700
taaccgctga agacattgtc cataaaatcg ctgccaggat ttatgaagaa 750
aatgacagag ccgtgtttga caagattgtt tctaaactac ttaatctcgg 800
ccttatcaca gaaagccaag cacatacact ggaagatgaa gtagcagagg 850
ttttacaaaa attaattctca aaggaagcca acaattatga ggaggatccc 900
aataagccca caagctggac tgagaatcag gctggaaaaa taccagagaa 950
agtgactcca atggcagcaa ttcaagatgg tcttgctaag ggagaaaacg 1000
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tttctatgcg ctactgaaaa gtattgattc agaaaaagaa gcaaaagaga 1150
aagaaacact gattactatc atgaaaacac tgattgactt tgtgaagatg 1200
atggtgaaat atggaacaat atctccagaa gaaggtgttt cctaccttga 1250
aaacttggat gaaatgattg ctcttcagac caaaaacaag ctagaaaaaa 1300
atgctactga caatataagc aagcttttcc cagcaccatc agagaagagt 1350
catgaagaaa cagacagtac caaggaagaa gcagctaaga tggaagga 1400
atatggaagc ttgaaggatt ccacaaaaga tgataactcc aaccaggag 1450
gaaagacaga tgaacccaaa ggaaaaacag aagcctattt ggaagccatc 1500

agaaaaaata ttgaatggtt gaagaaacat gacaaaaagg gaaataaaga 1550
 agattatgac ctttcaaaga tgagagactt catcaataaa caagctgatg 1600
 cttatgtgga gaaaggcatc cttgacaagg aagaagccga ggccatcaag 1650
 cgcatttata gcagcctgta aaaatggcaa aagatccagg agtcctttcaa 1700
 ctgtttcaga aacataata tagcttaaaa caotttcta tctgtgatta 1750
 aaatTTTTTg acccaagggt tattagaaag tgctgaattt acagtagtta 1800
 accttttaca agtggttaaa acatagcttt cttcccgtaa aaactatctg 1850
 aaagtaaagt tgtatgtaag ctgaaaaaaaa aaaaaaaaaa aaa 1893

<210> 67
 <211> 468
 <212> PRT
 <213> Homo Sapien

<400> 67
 Met Gly Phe Leu Gly Thr Gly Thr Trp Ile Leu Val Leu Val Leu
 1 5 10 15
 Pro Ile Gln Ala Phe Pro Lys Pro Gly Gly Ser Gln Asp Lys Ser
 20 25 30
 Leu His Asn Arg Glu Leu Ser Ala Glu Arg Pro Leu Asn Glu Gln
 35 40 45
 Ile Ala Glu Ala Glu Glu Asp Lys Ile Lys Lys Thr Tyr Pro Pro
 50 55 60
 Glu Asn Lys Pro Gly Gln Ser Asn Tyr Ser Phe Val Asp Asn Leu
 65 70 75
 Asn Leu Leu Lys Ala Ile Thr Glu Lys Glu Lys Ile Glu Lys Glu
 80 85 90
 Arg Gln Ser Ile Arg Ser Ser Pro Leu Asp Asn Lys Leu Asn Val
 95 100 105
 Glu Asp Val Asp Ser Thr Lys Asn Arg Lys Leu Ile Asp Asp Tyr
 110 115 120
 Asp Ser Thr Lys Ser Gly Leu Asp His Lys Phe Gln Asp Asp Pro
 125 130 135
 Asp Gly Leu His Gln Leu Asp Gly Thr Pro Leu Thr Ala Glu Asp
 140 145 150
 Ile Val His Lys Ile Ala Ala Arg Ile Tyr Glu Glu Asn Asp Arg
 155 160 165
 Ala Val Phe Asp Lys Ile Val Ser Lys Leu Leu Asn Leu Gly Leu
 170 175 180

Ile Thr Glu Ser	Gln Ala His Thr Leu	Glu Asp Glu Val Ala Glu	185	190	195
Val Leu Gln Lys	Leu Ile Ser Lys Glu	Ala Asn Asn Tyr Glu Glu	200	205	210
Asp Pro Asn Lys	Pro Thr Ser Trp Thr	Glu Asn Gln Ala Gly Lys	215	220	225
Ile Pro Glu Lys	Val Thr Pro Met Ala	Ala Ile Gln Asp Gly Leu	230	235	240
Ala Lys Gly Glu	Asn Asp Glu Thr Val	Ser Asn Thr Leu Thr Leu	245	250	255
Thr Asn Gly Leu	Glu Arg Arg Thr Lys	Thr Tyr Ser Glu Asp Asn	260	265	270
Phe Glu Glu Leu	Gln Tyr Phe Pro Asn	Phe Tyr Ala Leu Leu Lys	275	280	285
Ser Ile Asp Ser	Glu Lys Glu Ala Lys	Glu Lys Glu Thr Leu Ile	290	295	300
Thr Ile Met Lys	Thr Leu Ile Asp Phe	Val Lys Met Met Val Lys	305	310	315
Tyr Gly Thr Ile	Ser Pro Glu Glu Gly	Val Ser Tyr Leu Glu Asn	320	325	330
Leu Asp Glu Met	Ile Ala Leu Gln Thr	Lys Asn Lys Leu Glu Lys	335	340	345
Asn Ala Thr Asp	Asn Ile Ser Lys Leu	Phe Pro Ala Pro Ser Glu	350	355	360
Lys Ser His Glu	Glu Thr Asp Ser Thr	Lys Glu Glu Ala Ala Lys	365	370	375
Met Glu Lys Glu	Tyr Gly Ser Leu Lys	Asp Ser Thr Lys Asp Asp	380	385	390
Asn Ser Asn Pro	Gly Gly Lys Thr Asp	Glu Pro Lys Gly Lys Thr	395	400	405
Glu Ala Tyr Leu	Glu Ala Ile Arg Lys	Asn Ile Glu Trp Leu Lys	410	415	420
Lys His Asp Lys	Lys Gly Asn Lys Glu	Asp Tyr Asp Leu Ser Lys	425	430	435
Met Arg Asp Phe	Ile Asn Lys Gln Ala	Asp Ala Tyr Val Glu Lys	440	445	450
Gly Ile Leu Asp	Lys Glu Glu Ala Glu	Ala Ile Lys Arg Ile Tyr	455	460	465
Ser Ser Leu					

<210> 68
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 68
cgtcacagga acttcagcac cc 22

<210> 69
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 69
gtcttggtt cctccaggtt tgg 23

<210> 70
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 70
ggacagcgct cccctctacc tggagacttg actcccg 38

<210> 71
<211> 2379
<212> DNA
<213> Homo Sapien

<400> 71
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cgggccacca tggcgctgcc tccaggccca gccgccctcc ggcacacact 100
gctgctcctg ccagcccttc tgagctcagg ttggggggag ttggagccac 150
aaatagatgg tcagacctgg gctgagcggg cacttcggga gaatgaacgc 200
cacgccttca cctgccgggt ggcagggggg cctggcaccc ccagattggc 250
ctgggtatctg gatggacagc tgcaggaggc cagcacctca agactgctga 300
gcgtgggagg ggaggccttc tctggaggca ccagcacctt cactgtcact 350
gcccacgagg cccagcatga gctcaactgc tctctgcagg accccagaag 400
tggccgatca gccaacgcct ctgtcatcct taatgtgcaa ttcaagccag 450

agattgcccc agtcggcgcc aagtaccagg aagctcaggg ccagggcctc 500
 ctggttgtcc tgtttgccct ggtgctgccc aaccgcccgg ccaatgtcac 550
 ctggatcgac caggatgggc cagtgactgt caacacctct gacttcctgg 600
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 cagctccgca gcctggcaca caacctctcg gtggtggcca ccaatgacgt 700
 ggggtgcacc agtgcgtcgc ttccagcccc aggcccctcc cggcacccat 750
 ctctgatatc aagtgactcc aacaacctaa aactcaacaa cgtgcgcctg 800
 ccacgggaga acatgtccct ccggtccaac cttcagctca atgacctcac 850
 tccagattcc agagcagtga aaccagcaga ccggcagatg gtcagaaca 900
 acagccggcc agagcttctg gaccgggagc ccggcggcct cctcaccagc 950
 caaggtttca tccgcctccc agtgctgggc tatatctatc gagtgtccag 1000
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 tgtaaccgcg aggggcacag gtatctttgg caaggctacc agttggacgt 1250
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 aagtgtggca tggcctgctg tataccccac ccagtactc cacagcacct 1400
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tctgggattc actgtgagtg tcctgagctc tcgggggttga tggtttttct 1950
ctcagcatgt ctcctccacc acgggacccc agccctgacc aacccatggt 2000
tgcctcatca gcaggaaggt gcccttcctg gaggatgggc gccacaggca 2050
cataattcaa cagtgtggaa gctttagggg aacatggaga aagaaggaga 2100
ccacataccc caaagtgacc taagaacact ttaaaaagca acatgtaaat 2150
gattggaaat taatatagta cagaatatat ttttcccttg ttgagatctt 2200
cttttgtaat gtttttcatg ttactgccta gggcggtgct gagcacacag 2250
caagtttaat aaacttgact gaattcattt aaaaaaaaaa aaaaaaaaaa 2300
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2350
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2379

<210> 72
<211> 322
<212> PRT
<213> Homo Sapien

<400> 72
Met Ala Leu Pro Pro Gly Pro Ala Ala Leu Arg His Thr Leu Leu
1 5 10 15
Leu Leu Pro Ala Leu Leu Ser Ser Gly Trp Gly Glu Leu Glu Pro
20 25 30
Gln Ile Asp Gly Gln Thr Trp Ala Glu Arg Ala Leu Arg Glu Asn
35 40 45
Glu Arg His Ala Phe Thr Cys Arg Val Ala Gly Gly Pro Gly Thr
50 55 60
Pro Arg Leu Ala Trp Tyr Leu Asp Gly Gln Leu Gln Glu Ala Ser
65 70 75
Thr Ser Arg Leu Leu Ser Val Gly Gly Glu Ala Phe Ser Gly Gly
80 85 90
Thr Ser Thr Phe Thr Val Thr Ala His Arg Ala Gln His Glu Leu
95 100 105
Asn Cys Ser Leu Gln Asp Pro Arg Ser Gly Arg Ser Ala Asn Ala
110 115 120
Ser Val Ile Leu Asn Val Gln Phe Lys Pro Glu Ile Ala Gln Val
125 130 135
Gly Ala Lys Tyr Gln Glu Ala Gln Gly Pro Gly Leu Leu Val Val
140 145 150
Leu Phe Ala Leu Val Arg Ala Asn Pro Pro Ala Asn Val Thr Trp
155 160 165

Ile	Asp	Gln	Asp	Gly	Pro	Val	Thr	Val	Asn	Thr	Ser	Asp	Phe	Leu
				170					175					180
Val	Leu	Asp	Ala	Gln	Asn	Tyr	Pro	Trp	Leu	Thr	Asn	His	Thr	Val
				185					190					195
Gln	Leu	Gln	Leu	Arg	Ser	Leu	Ala	His	Asn	Leu	Ser	Val	Val	Ala
				200					205					210
Thr	Asn	Asp	Val	Gly	Val	Thr	Ser	Ala	Ser	Leu	Pro	Ala	Pro	Gly
				215					220					225
Pro	Ser	Arg	His	Pro	Ser	Leu	Ile	Ser	Ser	Asp	Ser	Asn	Asn	Leu
				230					235					240
Lys	Leu	Asn	Asn	Val	Arg	Leu	Pro	Arg	Glu	Asn	Met	Ser	Leu	Pro
				245					250					255
Ser	Asn	Leu	Gln	Leu	Asn	Asp	Leu	Thr	Pro	Asp	Ser	Arg	Ala	Val
				260					265					270
Lys	Pro	Ala	Asp	Arg	Gln	Met	Ala	Gln	Asn	Asn	Ser	Arg	Pro	Glu
				275					280					285
Leu	Leu	Asp	Pro	Glu	Pro	Gly	Gly	Leu	Leu	Thr	Ser	Gln	Gly	Phe
				290					295					300
Ile	Arg	Leu	Pro	Val	Leu	Gly	Tyr	Ile	Tyr	Arg	Val	Ser	Ser	Val
				305					310					315
Ser	Ser	Asp	Glu	Ile	Trp	Leu								
				320										

<210> 73
 <211> 843
 <212> DNA
 <213> Homo Sapien

<400> 73
 cggggacgga agcggcccct gggcccagag ggctggagcc gggccggggc 50
 gatgtggagc gcgggccgcg gcggggctgc ctggccggtg ctgttggggc 100
 tgctgctggc gctgttagtg ccgggcggtg gtgccgcaa gaccggtgcg 150
 gagctcgtga cctgcgggtc ggtgctgaag ctgctcaata cgcaccaccg 200
 cgtgcggctg cactcgcacg acatcaaata cggatccggc agcggccagc 250
 aatcggtgac cggcgtagag gcgtcggacg acgccaatag ctactggcgg 300
 atccgcggcg gctcggaggg cgggtgcccg cgcgggtccc cggtgcgctg 350
 cgggcaggcg gtgaggctca cgcatgtgct tacgggcaag aacctgcaca 400
 cgcaccactt cccgtcgccg ctgtccaaca accaggaggt gagtgccttt 450
 ggggaagacg gcgagggcga cgacctggac ctatggacag tgcgctgctc 500

tggacagcac tgggagcgtg aggctgctgt gcgcttccag catgtgggca 550
cctctgtgtt cctgtcagtc acgggtgagc agtatggaag ccccatccgt 600
gggcagcatg aggtccacgg catgcccagt gccaacacgc acaatacgtg 650
gaaggccatg gaaggcatct tcatcaagcc tagtgtggag ccctctgcag 700
gtcacgatga actctgagtg tgtggatgga tgggtggatg gaggggtggca 750
gggtggggcgt ctgcagggcc actcttggca gagactttgg gttttagagg 800
gtcctcaagt gcctttgtga ttaaagaatg ttggtctatg aaa 843

<210> 74
<211> 221
<212> PRT
<213> Homo Sapien

<400> 74
Met Trp Ser Ala Gly Arg Gly Gly Ala Ala Trp Pro Val Leu Leu
1 5 10 15
Gly Leu Leu Leu Ala Leu Leu Val Pro Gly Gly Gly Ala Ala Lys
20 25 30
Thr Gly Ala Glu Leu Val Thr Cys Gly Ser Val Leu Lys Leu Leu
35 40 45
Asn Thr His His Arg Val Arg Leu His Ser His Asp Ile Lys Tyr
50 55 60
Gly Ser Gly Ser Gly Gln Gln Ser Val Thr Gly Val Glu Ala Ser
65 70 75
Asp Asp Ala Asn Ser Tyr Trp Arg Ile Arg Gly Gly Ser Glu Gly
80 85 90
Gly Cys Pro Arg Gly Ser Pro Val Arg Cys Gly Gln Ala Val Arg
95 100 105
Leu Thr His Val Leu Thr Gly Lys Asn Leu His Thr His His Phe
110 115 120
Pro Ser Pro Leu Ser Asn Asn Gln Glu Val Ser Ala Phe Gly Glu
125 130 135
Asp Gly Glu Gly Asp Asp Leu Asp Leu Trp Thr Val Arg Cys Ser
140 145 150
Gly Gln His Trp Glu Arg Glu Ala Ala Val Arg Phe Gln His Val
155 160 165
Gly Thr Ser Val Phe Leu Ser Val Thr Gly Glu Gln Tyr Gly Ser
170 175 180
Pro Ile Arg Gly Gln His Glu Val His Gly Met Pro Ser Ala Asn
185 190 195

Thr His Asn Thr Trp Lys Ala Met Glu Gly Ile Phe Ile Lys Pro
 200 205 210

Ser Val Glu Pro Ser Ala Gly His Asp Glu Leu
 215 220

<210> 75
 <211> 1049
 <212> DNA
 <213> Homo Sapien

<400> 75
 gttgctatgt tgcccaggct ggtcttgaag tgccttgacc tcctaaagtg 50
 ttggaaccac agacgtgagc cactccaccc agcctaaaac ttcatcttct 100
 ttggatgaga tgaacacttt taacaagaga acaggactct atataaatcg 150
 ctgtgggctc accacctcta aggaggagca ctgactgaag acagaaaaat 200
 tgatgaactg aagaagacat ggtccattat gccttacaaa cttacacagt 250
 gctttgggaa ttccaaagta ctcagtggag agaggtgttt caggagccgt 300
 agagccagat cgtcatcatg tctgcattgt ggctgctgct gggcctcctt 350
 gccctgatgg acttgtctga aagcagcaac tggggatgct atggaaacat 400
 ccaaagcctg gacaccctg gagcatcttg tgggattgga agacgtcacg 450
 gcctgaacta ctgtggagtt cgtgcttctg aaaggctggc tgaaatagac 500
 atgccatacc tcctgaaata tcaacccatg atgcaaacca ttggccaaaa 550
 gtactgcatg gatcctgccg tgatcgctgg tgtcttgtcc aggaagtctc 600
 ccggtgacaa aattctggtc aacatgggag ataggactag catggtgcag 650
 gaccctggct ctcaagctcc cacatcctgg attagtgagt ctgaggtttc 700
 ccagacaact gaagttctga ctactagaat caaagaaatc cagaggaggt 750
 ttccaacctg gaccctgac cagtacctga gaggtggact ctgtgcctac 800
 agtgggggtg ctggctatgt ccgaagcagc caggacctga gctgtgactt 850
 ctgcaatgat gtccttgac gagccaagta cctcaagaga catggcttct 900
 aacatctcag atgaaacca agaccatgat cacatatgca gcctcaaagt 950
 ttacacagat aaaactagcc aagggcacct gtaactggga atctgagttt 1000
 gacctaaaag tcattaaaat aacatgaatc ccattaaaaa aaaaaaaaaa 1049

<210> 76
 <211> 194
 <212> PRT
 <213> Homo Sapien

<400> 76

Met Ser Ala Leu Trp Leu Leu Leu Gly Leu Leu Ala Leu Met Asp
1 5 10 15
Leu Ser Glu Ser Ser Asn Trp Gly Cys Tyr Gly Asn Ile Gln Ser
20 25 30
Leu Asp Thr Pro Gly Ala Ser Cys Gly Ile Gly Arg Arg His Gly
35 40 45
Leu Asn Tyr Cys Gly Val Arg Ala Ser Glu Arg Leu Ala Glu Ile
50 55 60
Asp Met Pro Tyr Leu Leu Lys Tyr Gln Pro Met Met Gln Thr Ile
65 70 75
Gly Gln Lys Tyr Cys Met Asp Pro Ala Val Ile Ala Gly Val Leu
80 85 90
Ser Arg Lys Ser Pro Gly Asp Lys Ile Leu Val Asn Met Gly Asp
95 100 105
Arg Thr Ser Met Val Gln Asp Pro Gly Ser Gln Ala Pro Thr Ser
110 115 120
Trp Ile Ser Glu Ser Gln Val Ser Gln Thr Thr Glu Val Leu Thr
125 130 135
Thr Arg Ile Lys Glu Ile Gln Arg Arg Phe Pro Thr Trp Thr Pro
140 145 150
Asp Gln Tyr Leu Arg Gly Gly Leu Cys Ala Tyr Ser Gly Gly Ala
155 160 165
Gly Tyr Val Arg Ser Ser Gln Asp Leu Ser Cys Asp Phe Cys Asn
170 175 180
Asp Val Leu Ala Arg Ala Lys Tyr Leu Lys Arg His Gly Phe
185 190

<210> 77

<211> 899

<212> DNA

<213> Homo Sapien

<400> 77

ttgaaaatct actctatcag ctgctgtggt tgccaccatt ctcaggaccc 50
tcgccatgaa agcccttatg ctgctcacc tgtctgttct gctctgctgg 100
gtctcagctg acattcgctg tcaactcctgc tacaaggtcc ctgtgctggg 150
ctgtgtggac cggcagtcct gccgcctgga gccaggacag caatgcctga 200
caacacatgc ataccttggt aagatgtggg ttttctccaa tctgcgctgt 250
ggcacaccag aagagccctg tcaggaggcc ttcaaccaa ccaaccgcaa 300

gctgggtctg acatataaca ccacctgctg caacaaggac aactgcaaca 350
gcgcaggacc ccggcccact ccagccctgg gccttgtctt ccttacctcc 400
ttggctggcc ttggcctctg gctgctgcac tgagactcat tccattggct 450
gcccctcttc ccacctgcct tggcctgagc ctctctccct gtgtctctgt 500
atccccctggc ttacagaat cgtctctccc tagctcccat ttctttaatt 550
aaacactggt ccgagtggtc tcctcatcca tccttcccac ctcacaccct 600
tcactctcct ttttctgggt cccttcccac ttccttccag gacctccatt 650
ggctcctaga agggctcccc actttgcttc ctatactctg ctgtccccta 700
cttgaggagg gattgggatc tgggcctgaa atggggcttc tgtgttgctc 750
ccagtgaagg ctcccacaag gacctgatga cctcactgta cagagctgac 800
tccccaaacc caggctccca tatgtacccc atccccata ctcacctctt 850
tccattttga gtaataaatg tctgagtctg gaaaaaaaaa aaaaaaaaaa 899

<210> 78
<211> 125
<212> PRT
<213> Homo Sapien

<400> 78
Met Lys Ala Leu Met Leu Leu Thr Leu Ser Val Leu Leu Cys Trp
1 5 10 15
Val Ser Ala Asp Ile Arg Cys His Ser Cys Tyr Lys Val Pro Val
20 25 30
Leu Gly Cys Val Asp Arg Gln Ser Cys Arg Leu Glu Pro Gly Gln
35 40 45
Gln Cys Leu Thr Thr His Ala Tyr Leu Gly Lys Met Trp Val Phe
50 55 60
Ser Asn Leu Arg Cys Gly Thr Pro Glu Glu Pro Cys Gln Glu Ala
65 70 75
Phe Asn Gln Thr Asn Arg Lys Leu Gly Leu Thr Tyr Asn Thr Thr
80 85 90
Cys Cys Asn Lys Asp Asn Cys Asn Ser Ala Gly Pro Arg Pro Thr
95 100 105
Pro Ala Leu Gly Leu Val Phe Leu Thr Ser Leu Ala Gly Leu Gly
110 115 120
Leu Trp Leu Leu His
125

<210> 79

<211> 1977
<212> DNA
<213> Homo Sapien

<400> 79

acgggcccga gcggcagtga cgtaggggtg gcgcacggat ccgttgccgc 50
tgcagctctg cagtcggggc gttccttcgc cgccgccagg ggtagcgggtg 100
tagctgcgca gcgtcgcgcg cgctaccgca cccaggttcg gcccgtaggc 150
gtctggcagc ccggcgccat cttcatcgag cgccatggcc gcagcctgcg 200
ggccgggagc ggccgggtac tgcttgctcc tcggcttgca tttgtttctg 250
ctgaccgcgg gccctgccct gggctggaac gaccctgaca gaatgttgct 300
gcgggatgta aaagctctta ccctccacta tgaccgctat accacctccc 350
gcaggctgga tcccatccca cagttgaaat gtgttgaggg cacagctggc 400
tgtgattctt ataccccaaa agtcatacag tgtcagaaca aaggctggga 450
tgggtatgat gtacagtggg aatgtaagac ggacttagat attgcataca 500
aatttgaaa aactgtggtg agctgtgaag gctatgagtc ctctgaagac 550
cagtatgtac taagagggtt ttgtggcttg gagtataatt tagattatac 600
agaacttggc ctgcagaaac tgaaggagtc tggaaagcag cacggctttg 650
cctctttctc tgattattat tataagtggc cctcggcgga ttctgtaac 700
atgagtggat tgattaccat cgtgggtact cttgggatcg cttttgtagt 750
ctataagctg ttcttgagtg acgggcagta ttctcctcca ccgtactctg 800
agtatcctcc attttccac cgttaccaga gattcaccaa ctacagcagga 850
cctcctcccc caggctttaa gtctgagttc acaggaccac agaatactgg 900
ccatgggtgca acttctggtt ttggcagtgc ttttacagga caacaaggat 950
atgaaaattc aggaccaggg ttctggacag gcttgggaac tgggtggaata 1000
ctaggatatt tgtttggcag caatagagcg gcaacaccct tctcagactc 1050
gtggtactac ccgtcctatc ctccctccta cctgggcacg tggaataggg 1100
cttactcacc ccttcatgga ggctcgggca gctattcggg atgttcaaac 1150
tcagacacga aaaccagaac tgcacagga tatggtggta ccaggagacg 1200
ataaagtaga aagttggagt caaacactgg atgcagaaat tttggatttt 1250
tcatacttt ctcttttaga aaaaagtact acctgttaac aattgggaaa 1300
aggggatatt caaaagttct gtggtgttat gtccagtgtg gctttttgta 1350

ttctattatt tgaggctaaa agttgatgtg tgacaaaata cttatgtggt 1400
 gtatgtcagt gtaacatgca gatgtatatt gcagtttttg aaagtgatca 1450
 ttactgtgga atgctaaaaa tacattaatt tctaaaacct gtgatgccct 1500
 aagaagcatt aagaatgaag gtgttgact aatagaaact aagtacagaa 1550
 aatttcagtt ttaggtgggt gtagctgatg agttattacc tcatagagac 1600
 tataatatcc tatttggtat tatattatgt gatgtttgct gttcttcaaa 1650
 catttaaatt aagctttgga ctaattatgc taatttgatga gttctgatca 1700
 cttttgagct ctgaagcttt gaatcattca gtggtggaga tggccttctg 1750
 gtaactgaat attaccttct gtaggaaaag gtggaaaata agcatctaga 1800
 aggttggtgt gaatgactct gtgctggcaa aaatgcttga aacctctata 1850
 tttctttcgt tcataagagg taaaggtcaa atttttcaac aaaagtcttt 1900
 taataacaaa agcatgcagt tctctgtgaa atctcaaata ttgttgtaat 1950
 agtctgtttc aatcttaaaa agaata 1977

<210> 80
 <211> 339
 <212> PRT
 <213> Homo Sapien

<400> 80
 Met Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu
 1 5 10 15
 Leu Gly Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly
 20 25 30
 Trp Asn Asp Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu
 35 40 45
 Thr Leu His Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro
 50 55 60
 Ile Pro Gln Leu Lys Cys Val Gly Gly Thr Ala Gly Cys Asp Ser
 65 70 75
 Tyr Thr Pro Lys Val Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly
 80 85 90
 Tyr Asp Val Gln Trp Glu Cys Lys Thr Asp Leu Asp Ile Ala Tyr
 95 100 105
 Lys Phe Gly Lys Thr Val Val Ser Cys Glu Gly Tyr Glu Ser Ser
 110 115 120
 Glu Asp Gln Tyr Val Leu Arg Gly Ser Cys Gly Leu Glu Tyr Asn
 125 130 135

Leu	Asp	Tyr	Thr	Glu	Leu	Gly	Leu	Gln	Lys	Leu	Lys	Glu	Ser	Gly	140	145	150
Lys	Gln	His	Gly	Phe	Ala	Ser	Phe	Ser	Asp	Tyr	Tyr	Tyr	Lys	Trp	155	160	165
Ser	Ser	Ala	Asp	Ser	Cys	Asn	Met	Ser	Gly	Leu	Ile	Thr	Ile	Val	170	175	180
Val	Leu	Leu	Gly	Ile	Ala	Phe	Val	Val	Tyr	Lys	Leu	Phe	Leu	Ser	185	190	195
Asp	Gly	Gln	Tyr	Ser	Pro	Pro	Pro	Tyr	Ser	Glu	Tyr	Pro	Pro	Phe	200	205	210
Ser	His	Arg	Tyr	Gln	Arg	Phe	Thr	Asn	Ser	Ala	Gly	Pro	Pro	Pro	215	220	225
Pro	Gly	Phe	Lys	Ser	Glu	Phe	Thr	Gly	Pro	Gln	Asn	Thr	Gly	His	230	235	240
Gly	Ala	Thr	Ser	Gly	Phe	Gly	Ser	Ala	Phe	Thr	Gly	Gln	Gln	Gly	245	250	255
Tyr	Glu	Asn	Ser	Gly	Pro	Gly	Phe	Trp	Thr	Gly	Leu	Gly	Thr	Gly	260	265	270
Gly	Ile	Leu	Gly	Tyr	Leu	Phe	Gly	Ser	Asn	Arg	Ala	Ala	Thr	Pro	275	280	285
Phe	Ser	Asp	Ser	Trp	Tyr	Tyr	Pro	Ser	Tyr	Pro	Pro	Ser	Tyr	Pro	290	295	300
Gly	Thr	Trp	Asn	Arg	Ala	Tyr	Ser	Pro	Leu	His	Gly	Gly	Ser	Gly	305	310	315
Ser	Tyr	Ser	Val	Cys	Ser	Asn	Ser	Asp	Thr	Lys	Thr	Arg	Thr	Ala	320	325	330
Ser	Gly	Tyr	Gly	Gly	Thr	Arg	Arg	Arg							335		